

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## (i) APPLICANT:

(A) NAME: BRIGHAM AND WOMEN'S HOSPITAL  
(B) STREET: 75 FRANCIS STREET  
(C) CITY: BOSTON  
(D) STATE: MASSACHUSETTS  
(E) COUNTRY: USA  
(F) POSTAL CODE (ZIP): 02115  
(A) NAME: DANA-FARBER CANCER INSTITUTE  
(B) STREET: 44 BINNEY STREET  
(C) CITY: BOSTON  
(D) STATE: MASSACHUSETTS  
(E) COUNTRY: USA  
(F) POSTAL CODE (ZIP): 02115

(ii) TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules  
and Uses Therefor

(iii) NUMBER OF SEQUENCES: 65

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: LAHIVE & COCKFIELD  
(B) STREET: 60 State Street, suite 510  
(C) CITY: Boston  
(D) STATE: Massachusetts  
(E) COUNTRY: USA  
(F) ZIP: 02109-1875

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: ASCII Text

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:

## (vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/205,697  
(B) FILING DATE: 02-Mar-1994

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Mandragouras, Amy E.  
(B) REGISTRATION NUMBER: 36,207  
(C) REFERENCE/DOCKET NUMBER: BWI-120CPPC

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 227-7400  
(B) TELEFAX: (617) 227-5941

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1888 base pairs

960220 52520780

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

10 (A) NAME/KEY: CDS  
 (B) LOCATION: 249..1208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

15 GAGTTTATA CCTCAATAGA CTCTTACTAG TTTCTCTTTT TCAGGTTGTG AAACTCAACC 60  
 TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG 120  
 20 TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTGTG GAGCCTAGGA 180  
 GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTT TCCAAAGCAT 240  
 CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC 290  
 Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu  
 1 5 10  
 AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT 338  
 Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg  
 15 20 25 30  
 CTT TCA CAA GTG TCT TCA GAT GTT GAT GAA CAA CTG TCC AAG TCA GTG 386  
 Leu Ser Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val  
 35 35 40 45  
 AAA GAT AAG GTA TTG CTG CCT TGC CGT TAC AAC TCT CCT CAT GAA GAT 434  
 Lys Asp Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp  
 50 55 60  
 GAG TCT GAA GAC CGA ATC TAC TGG CAA AAA CAT GAC AAA GTG GTG CTG 482  
 Glu Ser Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu  
 65 70 75  
 TCT GTC ATT GCT GGG AAA CTA AAA GTG TGG CCC GAG TAT AAG AAC CGG 530  
 Ser Val Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg  
 45 80 85 90  
 ACT TTA TAT GAC AAC ACT ACC TAC TCT CTT ATC ATC CTG GGC CTG GTC 578  
 Thr Leu Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val  
 95 100 105 110  
 CTT TCA GAC CGG GGC ACA TAC AGC TGT GTC GTT CAA AAG AAG GAA AGA 626  
 Leu Ser Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg  
 115 120 125  
 55 GGA ACG TAT GAA GTT AAA CAC TTG GCT TTA GTA AAG TTG TCC ATC AAA 674  
 Gly Thr Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys  
 130 135 140

03702525-03702525-03702525

	GCT GAC TTC TCT ACC CCC AAC ATA ACT GAG TCT GGA AAC CCA TCT GCA Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro Ser Ala 145 150 155	722
5	GAC ACT AAA AGG ATT ACC TGC TTT GCT TCC GGG GGT TTC CCA AAG CCT Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro Lys Pro 160 165 170	770
10	CGC TTC TCT TGG TTG GAA AAT GGA AGA GAA TTA CCT GGC ATC AAT ACG Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr 175 180 185 190	818
15	ACA ATT TCC CAG GAT CCT GAA TCT GAA TTG TAC ACC ATT AGT AGC CAA Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln 195 200 205	866
20	CTA GAT TTC AAT ACG ACT CGC AAC CAC ACC ATT AAG TGT CTC ATT AAA Leu Asp Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu Ile Lys 210 215 220	914
25	TAT GGA GAT GCT CAC GTG TCA GAG GAC TTC ACC TGG GAA AAA CCC CCA Tyr Gly Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro 225 230 235	962
30	GAA GAC CCT CCT GAT AGC AAG AAC ACA CTT GTG CTC TTT GGG GCA GGA Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly 240 245 250	1010
35	TTC GGC GCA GTA ATA ACA GTC GTC GTC ATC GTT GTC ATC ATC AAA TGC Phe Gly Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys 255 260 265 270	1058
40	TTC TGT AAG CAC GGT CTC ATC TAC CAT TTG CAA CTG ACC TCT TCT GCA Phe Cys Lys His Gly Leu Ile Tyr His Leu Gln Leu Thr Ser Ser Ala 275 280 285	1106
45	AAG GAC TTC AGA AAC CTA GCA CTA CCC TGG CTC TGC AAA CAC GGT TCT Lys Asp Phe Arg Asn Leu Ala Leu Pro Trp Leu Cys Lys His Gly Ser 290 295 300	1154
50	CTA GGT GAA GCC TCT GCA GTG ATT TGC AGA AGT ACT CAG ACG AAT GAA Leu Gly Glu Ala Ser Ala Val Ile Cys Arg Ser Thr Gln Thr Asn Glu 305 310 315	1202
55	CCA CAG TAGTTCTGCT GTTTCTGAGG ACGTAGTTTA GAGACTGAAT TCTTTGAAA Pro Gln 320	1258
60	GGACATAGGG ACAGTTTGCA CATTTGCTTG CACATCACAC ACACACACAC ACACACACAC 1318	
65	ACACACACAC ACACACACAC ACACACACAC ACACACACAC TCTCTCTCTC TCTCTCTCTC 1378	
70	GATACCTTAG GATAGGGTTC TACCCTGTTG CTCAGTGACA AAGAATCACT CTGTGGCGGA 1438	
75	GGCAGGCTTC AAGCTTGCAG CAATCCTCCT GCACCAGTTT CCTGAGTGCC AGACTTCCAG 1498	
80	GTGTAAGCTA TGGCACTTAG CAGAACAATA GCTGAATCAA TGAAGACACT GAGGTTCCAA 1558	
85	GAGGGAACCT GAATTATGAA GGTGAGTCAG AATCCAGATT TCCTGGCTCT ACCACTCTTA 1618	

960E00052520280

5 ACCTGTATCT GTTAGACCCC AAGCTCTGAG CTCATAGACA AGCTAATTTA AAATGCTTTT 1678  
 TAATAAGCAG AAGGCTCAGT TAGTACGGGG TTCAGGATAC TGCTTACTGG CAATATTTGA 1738  
 CTAGCCTCTA TTTTGTGTTGT TTTTAAAGG CCTACTGACT GTAGTGTAAAT TTGTAGGAAA 1798  
 CATGTTGCTA TGTATACCCA TTTGAGGGTA ATAAAAATGT TGGTAATTTT CAGCCAGCAC 1858  
 10 TTTCCAGGTA TTTCCCTTTT TATCCTTCAT 1888

## (2) INFORMATION FOR SEQ ID NO:2:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 320 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

25 Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe  
 1 5 10 15  
 Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg Leu Ser  
 20 25 30  
 30 Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val Lys Asp  
 35 40 45  
 Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp Glu Ser  
 50 55 60  
 35 Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu Ser Val  
 65 70 75 80  
 40 Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg Thr Leu  
 85 90 95  
 Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val Leu Ser  
 100 105 110  
 45 Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg Gly Thr  
 115 120 125  
 Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys Ala Asp  
 130 135 140  
 50 Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro Ser Ala Asp Thr  
 145 150 155 160  
 55 Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro Lys Pro Arg Phe  
 165 170 175  
 Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr Thr Ile  
 180 185 190

960E80-59520280  
 0870255-083096

Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln Leu Asp  
195 200 205

Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu Ile Lys Tyr Gly  
210 215 220

Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro Glu Asp  
225 230 235 240

Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly Phe Gly  
245 250 255

Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys Phe Cys  
260 265 270

Lys His Gly Leu Ile Tyr His Leu Gln Leu Thr Ser Ser Ala Lys Asp  
275 280 285

Phe Arg Asn Leu Ala Leu Pro Trp Leu Cys Lys His Gly Ser Leu Gly  
290 295 300

Glu Ala Ser Ala Val Ile Cys Arg Ser Thr Gln Thr Asn Glu Pro Gln  
305 310 315 320

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 249..1166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAGTTTATA CCTCAATAGA CTCTTACTAG TTTCTCTTTT TCAGGTTGTG AAACCTCAACC 60  
TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG 120  
TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTGTG GAGCCTAGGA 180  
GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTC TCCAAAGCAT 240  
CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC 290  
Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu  
1 5 10  
AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG AAT CGT 338  
Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Asn Arg  
15 20 25 30

08702555 0083096 960E80 52520/80

	CTT TCA CAA GTG TCT TCA GAT GTT GAT GAA CAA CTG TCC AAG TCA GTG Leu Ser Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val	386
	35 40 45	
5	AAA GAT AAG GTA TTG CTG CCT TGC CGT TAC AAC TCT CCT CAT GAA GAT Lys Asp Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp	434
	50 55 60	
10	GAG TCT GAA GAC CGA ATC TAC TGG GAA AAA CAT GAC AAA GTG GTG CTG Glu Ser Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu	482
	65 70 75	
15	TCT GTC ATT GCT GGG AAA CTA AAA GTG TGG CCC GAG TAT AAG AAC CGG Ser Val Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg	530
	80 85 90	
20	ACT TTA TAT GAC AAC ACT ACC TAC TCT CTT ATC ATC CTG GGC CTG GTC Thr Leu Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val	578
	95 100 105 110	
25	CTT TCA GAC CGG GGC ACA TAC AGC TGT GTC GTT CAA AAG AAG GAA AGA Leu Ser Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg	626
	115 120 125	
30	GGA ACG TAT GAA GTT AAA CAC TTG GCT TTA GTA AAG TTG TCC ATC AAA Gly Thr Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys	674
	130 135 140	
35	GCT GAC TTC TCT ACC CCC AAC ATA ACT GAG TCT GGA AAC CCA TCT GCA Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro Ser Ala	722
	145 150 155	
40	GAC ACT AAA AGG ATT ACC TGC TTT GCT TCC GGG GGT TTC CCA AAG CCT Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser Gly Glu Phe Pro Lys Pro	770
	160 165 170	
45	CGC TTC TCT TGG TTG GAA AAT GGA AGA GAA TTA CCT GGC ATC AAT ACG Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr	818
	175 180 185 190	
50	ACA ATT TCC CAG GAT CCT GAA TCT GAA TTG TAC ACC ATT AGT AGC CAA Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln	866
	195 200 205	
55	CTA GAT TTC AAT ACG ACT CGC AAC CAC ACC ATT AAG TGT CTC ATT AAA Leu Asp Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu Ile Lys	914
	210 215 220	
60	TAT GGA GAT GCT CAC GTG TCA GAG GAC TTC ACC TGG GAA AAA CCC CCA Tyr Gly Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro	962
	225 230 235	
65	GAA GAC CCT CCT GAT AGC AAG AAC ACA CTT GTG CTC TTT GGG GCA GGA Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Phe Gly Ala Gly	1010
	240 245 250	
70	TTC GGC GCA GTA ATA ACA GTC GTC GTC ATC GTT GTC ATC ATC AAA TGC Phe Gly Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys	1058
	255 260 265 270	

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5	TTC TGT AAG CAC AGA AGC TGT TTC AGA AGA AAT GAG GCA AGC AGA GAA Phe Cys Lys His Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser Arg Glu 275 280 285	1106
10	ACA AAC AAC AGC CTT ACC TTC GGG CCT GAA GAA GCA TTA GCT GAA CAG Thr Asn Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln 290 295 300	1154
15	ACC GTC TTC CTT TAGTTCTTCT CTGTCCATGT GGGATACATG GTATTATGTG Thr Val Phe Leu 305	1206
20	GCTCATGAGG TACAATCTTT CTTTCAGCAC CGTGCTAGCT GATCTTTCGG ACAACTTGAC ACAAGATAGA GTTAACTGGG AAGAGAAAGC CTTGAATGAG GATTTCTTTC CATCAGGAAG CTACGGGCAA GTTTGCTGGG CCTTTGATTG CTTGATGACT GAAGTGGAAA GGCTGAGCCC ACTGTGGGTG GTGCTAGCCC TGGGCAGGGG CAGGTGACCC TGGGTGGTAT AAGAAAAGA GCTGTCACTA AAAGGAGAGG TGCCTAGTCT TACTGCAACT TGATATGTCA TGTTTGGTTG GTGTCTGTGG GAGGCCTGCC CTTTTCTGAA GAGAAGTGGT GGGAGAGTGG ATGGGGTGGG GGCAGAGGAA AAGTGGGGGA GAGGGCCTGG GAGGAGAGGA GGGAGGGGGA CGGGGTGGGG GTGGGGAAAA CTATGGTTGG GATGTAAAAA CGGATAATAA TATAAATATT AAATAAAAAG AGAGTATTGA GCGGTCTCAT CTACCATTG CAACTGACCT CTTCTGCAAA GGAAGTTCAGA AACCTAGCAC TACCCTGGCT CTGCAAACAC GGTTCCTCTAG GTGAAGCCTC TGCAGTGATT TGCAGAAGTA CTCAGACGAA TGAACCACAG TAGTTCTGCT GTTTCTGAGG ACGTAGTTTA GAGACTGAAT TCTTTGGAAA GGACATAGGG ACAGTTTGCA CATTTGCTTG CACATCACAC ACACACACAC ACACACACAC ACACACACAC ACACACACAC ACACACACAC ACACACACAC TCTCTCTCTC TCTCTCTCTC GATACCTTAG GATAGGGTTC TACCCTGTTG CTCAGTGACA AAGAATCACT CTGTGGCGGA GGCAGGCTTC AAGCTTGACG CAATCCTCCT GCACCAGTTT CCTGAGTGCC AGACTTCCAG GTGTAAGCTA TGGCACTTAG CAGAACACTA GCTGAATCAA TGAAGACACT GAGGTTCCAA GAGGGAACCT GAATTATGAA GGTGAGTCAG AATCCAGATT TCCTGGCTCT ACCACTCTTA ACCTGTATCT GTTAGACCCC AAGCTCTGAG CTCATAGACA AGCTAATTTA AAATGCTTTT TAATAAGCAG AAGGCTCAGT TAGTACGGGG TTCAGGATAC TGCTTACTGG CAATATTTGA CTAGCCTCTA TTTTGTFTGT TTTTAAAGG CCTACTGACT GTAGTGTAAT TTGTAGGAAA CATGTTGCTA TGTATACCCA TTTGAGGGTA ATAAAAATGT TGGTAATTTT CAGCCAGCAC TTTCCAGGTA TTTCCCTTTT TATCCTTCAT	1266 1326 1386 1446 1506 1566 1626 1686 1746 1806 1866 1926 1986 2046 2106 2166 2226 2286 2346 2406 2466 2516

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..138

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGT CTC ATC TAC CAT TTG CAA CTG ACC TCT TCT GCA AAG GAC TTC AGA 48  
 Gly Leu Ile Tyr His Leu Gln Leu Thr Ser Ser Ala Lys Asp Phe Arg  
 1 5 10 15

AAC CTA GCA CTA CCC TGG CTC TGC AAA CAC GGT TCT CTA GGT GAA GCC 96  
 Asn Leu Ala Leu Pro Trp Leu Cys Lys His Gly Ser Leu Gly Glu Ala  
 20 25 30

TCT GCA GTG ATT TGC AGA AGT ACT CAG ACG AAT GAA CCA CAG 138  
 Ser Ala Val Ile Cys Arg Ser Thr Gln Thr Asn Glu Pro Gln  
 35 40 45

TAGTTCTGCT GTTCTGAGG ACGTAGTTTA GAGACTGAAT TCTTTGGAAA GGACATAGGG 198

ACAGTTTGCA CATTTGCTTG CACATCACAC ACACACACAC ACACACACAC ACACACACAC 258

ACACACACAC ACACACACAC ACACACACAC TCTCTCTCTC TCTCTCTCTC GATACCTTAG 318

GATAGGGTTC TACCCTGTTG CTCAGTGACA AAGAATCACT CTGTGGCGGA GGCAGGCTTC 378

AAGCTTGCAG CAATCCTCCT GCACCAGTTT CCTGAGTGCC AGACTTCCAG GTGTAAGCTA 438

TGGCACTTAG CAGAACACTA GCTGAATCAA TGAAGACACT GAGGTTCCAA GAGGGAACCT 498

GAATTATGAA GGTGAGTCAG AATCCAGATT TCCTGGCTCT ACCACTCTTA ACCTGTATCT 558

GTTAGACCCC AAGCTCTGAG CTCATAGACA AGCTAATTTA AAATGCTTTT TAATAAGCAG 618

AAGGCTCAGT TAGTACGGGG TTCAGGATAC TGCTTACTGG CAATATTGTA CTAGCCTCTA 678

TTTTGTTTGT TTTTAAAGG CCTACTGACT GTAGTGTAAT TTGTAGGAAA CATGTTGCTA 738

TGTATACCCA TTTGAGGGTA ATAAAAATGT TGGTAATTTT CAGCCAGCAC TTTCCAGGTA 798

TTTCCCTTTT TATCCTTCAT 818

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids  
 (B) TYPE: amino acid

0870555 083030 52520280

8b35  
8a1



(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Gly Leu Ile Tyr His Leu Gln Leu Thr Ser Ser Ala Lys Asp Phe Arg  
 1 5 10 15

Asn Leu Ala Leu Pro Trp Leu Cys Lys His Gly Ser Leu Gly Glu Ala  
 20 25 30

Ser Ala Val Ile Cys Arg Ser Thr Gln Thr Asn Glu Pro Gln  
 35 40 45

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1753 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

50  
 30  
 35  
 40  
 45  
 50  
 55

GTTT TAGTAA CCAGAGGCCG CAAGAAGAGA TCACTTGTAT ATACACGGGC CCCATCTTTT 60  
 GCTTTT TAAG ACAAAGAAA AAGAATCTTC TTCAACAAGT AAGTAAATGC ATTTACTATT 120  
 TATCATGCTA TGGGACACCT TAGTAGAACA CGCTATCTCC AGCCTTATCA TATGCATATT 180  
 TTGTTGTTGT TGTGTTGTT GTTGTTAAAG ACAGGGTCTC ATATATGCCA GGCTGGTCCC 240  
 AAAC TTTCAG TGTAACCCAA GATAATCTGG AACTCCCGAC TCCTCTGCTC CCACCTCTCC 300  
 AGTGCAGGAC ACTGTTTATA CCGTGCTGGG GAATTGAACT CAGAGCACCC TGCATGTCAG 360  
 CTAAGCATTC TACCGACCAA GTCCCATGCC CAGTCCCTAA CTCCCCAACT TCACTGCTTT 420  
 TTAAACATAC ATACAATCAT AACTTGCCCT CAGAGCAGTC TCCTGGGGTC TCTTATTCTC 480  
 AAGGCTGCGG CATTCCAACA CTGTTAGAAA AACACCATCA GGATTCTTTT GTGTTTCCTA 540  
 GATGCAAACA TTTTGTAGG GCGAAGTTGA GGTTTTCTA ATCAAGAAAA TGCCGGTAAC 600  
 AAGTCTCTTC AAGCTAACTG GTTGGCTAAG GGGTATCTCT CCAAAGAAG AGATCCACAT 660  
 GTCAGGCCAG TTGTAGGCAT GATGTCAGGT CTCCCTCCCT TTCTTCTTT CTTTCTTTT 720  
 TTCTTCTTT CTTTTTTTCT TTCTTCTTA CTTTCTTACT TTCTTCTTT TCTGTTTTT 780  
 GGTTTTTCGA GACAGGGTTT CTTTGTATAG CCCTGGCTGT CCTGGAAGTC GCTCTGTAGA 840  
 CCAGGCTGGC CTCGAACTCA GAAATCTGCC TCTGCCTTTA CCTCCTGAGT GCTGGGAATT 900  
 AAAGGTGTGC ACCACCATGC CCGGCTGGGA TGTCATTCGT TTTCATTCT CAATTTTGAT 960

08702525-03700

ACTTTATGGA AGAAAAAAGA AAAGATAGAC AAGCCTCTTC ATGTAATACC CCATAGTCTC 1020  
AATAAGTGGT GTTCGTAACG TGGCTTCTCT TTCCTTACCT TTTACTGGTA GATTTCTCGG 1080  
TTGATTGATG TCCCTGTAGG ACTTACTGGG TTTAAGATTC TTGGTTTCCT GTTTTAAGAT 1140  
ATAAAGAAAC CATTTCCTAA CTAAACACT GCCTTGACAA AATATACTTT TGGCAGTCAC 1200  
TCTGTGTCCA GAATGGAATT TAAGCTTTCA TGGCCTAGCT GCTAGTGAAG GTTCTTTGCT 1260  
TTTTTTTGGC TGTTGTATGT GAAATGGGGT TGGGTGGGAA CCACCTCACT GTGTTCTAGT 1320  
GTTAGTCACC CCACCCCCGC AAGCAGAATC CTTTACCCA GCTTTTTCAC CCAGCTGTGC 1380  
TCACCCGGTG CTCAGAACAG GCCTGGACAA GTCAGCTCCC CTAGAGTTCT GGGGACCTTT 1440  
GAGTTGCCCT CATGGCCACA CCCTGATTCA GAACTCTCAC TCTGTCGTAA GATAGAGCTA 1500  
CTGGGGAGTT TTATACCTCA ATAGACTCTT ACTAGTTTCT CTTTTCAGG TTGTGAAACT 1560  
CAACCTTCAA AGACACTCTG TTCCATTCTT GTGGACTAAT AGGATCATCT TTAGCATCTG 1620  
CCGGGTGGAT GCCATCCAGG CTTCTTTTTC TACATCTCTG TTTCTCGATT TTTGTGAGCC 1680  
TAGGAGGTGC CTAAGCTCCA TTGGCTCTAG ATTCCTGGCT TTCCCCATCA TGTTCTCCAA 1740  
AGCATCTGAA GCT 1753

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TGTCCAGGCA GAGCTAGTGG CTGCCCCTAG CGCTTCCTCT TCTTTGATAC CCCAAAGTCT 60  
GAGTTTATTA CACATCCTTG GTGACCAAAT CACATGGGAG CTTCTCCGA GGTCTTAGTA 120  
AAGGGAAGTT GGAAAGGGGA AATTCCTGCC CCCCTGCC 158

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1398 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS

(B) LOCATION: 249..848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

5 GAGTTTATA CCTCAATAGA CTCTTACTAG TTTCTCTTTT TCAGGTTGTG AAACCTCAACC 60  
 TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG 120  
 10 TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTGTG GAGCCTAGGA 180  
 GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTC TCCAAAGCAT 240  
 15 CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC 290  
 Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu  
 1 5 10  
 AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT 338  
 Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg  
 20 15 20 25 30  
 CTT TCA CAA GTG TCT TCA GCT GAC TTC TCT ACC CGC AAC ATA ACT GAG 386  
 Leu Ser Gln Val Ser Ser Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu  
 35 40 45  
 25 TCT GGA AAC CCA TCT GCA GAC ACT AAA AGG ATT ACC TGC TTT GCT TCC 434  
 Ser Gly Asn Pro Ser Ala Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser  
 50 55 60  
 30 GGG GGT TTC CCA AAG CCT CGC TTC TCT TGG TGG GAA AAT GGA AGA GAA 482  
 Gly Gly Phe Pro Lys Pro Arg Phe Ser Trp Trp Glu Asn Gly Arg Glu  
 65 70 75  
 35 TTA CCT GGC ATC AAT ACG ACA ATT TCC CAG GAT CCT GAA TCT GAA TTG 530  
 Leu Pro Gly Ile Asn Thr Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu  
 80 85 90  
 TAC ACC ATT AGT AGC CAA CTA GAT TTC AAT ACG ACT CGC AAC CAC ACC 578  
 Tyr Thr Ile Ser Ser Gln Leu Asp Phe Asn Thr Thr Arg Asn His Thr  
 40 95 100 105 110  
 ATT AAG TGT CTC ATT AAA TAT GGA GAT GCT CAC GTG TCA GAG GAC TTC 626  
 Ile Lys Cys Leu Ile Lys Tyr Gly Asp Ala His Val Ser Glu Asp Phe  
 115 120 125  
 45 ACC TGG GAA AAA CCC CCA GAA GAC CCT CCT GAT AGC AAG AAC ACA CTT 674  
 Thr Trp Glu Lys Pro Pro Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu  
 130 135 140  
 50 GTG CTC TTT GGG GCA GGA TTC GGC GCA GTA ATA ACA GTC GTC GTC ATC 722  
 Val Leu Phe Gly Ala Gly Phe Gly Ala Val Ile Thr Val Val Val Ile  
 145 150 155  
 55 GTT GTC ATC ATC AAA TGC TTC TGT AAG CAC AGA AGC TGT TTC AGA AGA 770  
 Val Val Ile Ile Lys Cys Phe Cys Lys His Arg Ser Cys Phe Arg Arg  
 160 165 170

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AAT GAG GCA AGC AGA GAA ACA AAC AAC AGC CTT ACC TTC GGG CCT GAA 818  
 Asn Glu Ala Ser Arg Glu Thr Asn Asn Ser Leu Thr Phe Gly Pro Glu  
 175 180 185 190  
 5 GAA GCA TTA GCT GAA CAG ACC GTC TTC CTT TAGTTCTTCT CTGTCCATGT 868  
 Glu Ala Leu Ala Glu Gln Thr Val Phe Leu  
 195 200  
 10 GGGATACATG GTATTATGTG GCTCATGAGG TACAATCTTT CTTTCAGCAC CGTGCTAGCT 928  
 GATCTTTCGG ACAACTTGAC ACAAGATAGA GTTAACTGGG AAGAGAAAGC CTTGAATGAG 988  
 GATTTCTTTC CATCAGGAAG CTACGGGCAA GTTTGCTGGG CCTTTGATTG CTTGATGACT 1048  
 15 GAAGTGGAAG GGCTGAGCCC ACTGTGGGTG GTGCTAGCCC TGGGCAGGGG CAGGTGACCC 1108  
 TGGGTGGTAT AAGAAAAAGA GCTGTCACTA AAAGGAGAGG TGCCTAGTCT TACTGCAACT 1168  
 20 TGATATGTCA TGTTTGTTG GTGTCTGTGG GAGGCCTGCC CTTTCTGAA GAGAAGTGGT 1228  
 GGGAGAGTGG ATGGGGTGGG GGCAGAGGAA AAGTGGGGGA GAGGCCTGG GAGGAGAGGA 1288  
 GGGAGGGGGA CGGGGTGGGG GTGGGGAAAA CTATGGTTGG GATGTAAAAA CGGATAATAA 1348  
 25 TATAAATATT AAATAAAAAG AGAGTATTGA GCAAAAAAAA AAAAAAAA 1398

## (2) INFORMATION FOR SEQ ID NO:9:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 200 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

40 Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe  
 1 5 10 15  
 Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg Leu Ser  
 20 25 30  
 45 Gln Val Ser Ser Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly  
 35 40 45  
 Asn Pro Ser Ala Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly  
 50 55 60  
 Phe Pro Lys Pro Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro  
 65 70 75 80  
 55 Gly Ile Asn Thr Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr  
 85 90 95  
 Ile Ser Ser Gln Leu Asp Phe Asn Thr Thr Arg Asn His Thr Ile Lys  
 100 105 110

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Cys Leu Ile Lys Tyr Gly Asp Ala His Val Ser Glu Asp Phe Thr Trp  
115 120 125

Glu Lys Pro Pro Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu  
130 135 140

Phe Gly Ala Gly Phe Gly Ala Val Ile Thr Val Val Val Ile Val Val  
145 150 155 160

Ile Ile Lys Cys Phe Cys Lys His Arg Ser Cys Phe Arg Arg Asn Glu  
165 170 175

Ala Ser Arg Glu Thr Asn Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala  
180 185 190

Leu Ala Glu Gln Thr Val Phe Leu  
195 200

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1570 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 249..890

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GAGTTTATA CCTCAATAGA CTCTTACTAG TTTCTCTTTT TCAGGTTGTG AAACCTCAACC 60

TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG 120

TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTGTG GAGCCTAGGA 180

GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTC TCCAAAGCAT 240

CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC 290  
Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu  
1 5 10

AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT 338  
Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg  
15 20 25 30

CTT TCA CAA GTG TCT TCA GCT GAC TTC TCT ACC CCC AAC ATA ACT GAG 386  
Leu Ser Gln Val Ser Ser Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu  
35 40 45

TCT GGA AAC CCA TCT GCA GAC ACT AAA AGG ATT ACC TGC TTT GCT TCC 434  
Ser Gly Asn Pro Ser Ala Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser  
50 55 60

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5	GGG GGT TTC CCA AAG CCT CGC TTC TCT TGG TTG GAA AAT GGA AGA GAA Gly Gly Phe Pro Lys Pro Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu 65 70 75	482
10	TTA CCT GGC ATC AAT ACG ACA ATT TCC CAG GAT CCT GAA TCT GAA TTG Leu Pro Gly Ile Asn Thr Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu 80 85 90	530
15	TAC ACC ATT AGT AGC CAA CTA GAT TTC AAT ACG ACT CGC AAC CAC ACC Tyr Thr Ile Ser Ser Gln Leu Asp Phe Asn Thr Thr Arg Asn His Thr 95 100 105 110	578
20	ATT AAG TGT CTC ATT AAA TAT GGA GAT GCT CAC GTG TCA GAG GAC TTC Ile Lys Cys Leu Ile Lys Tyr Gly Asp Ala His Val Ser Glu Asp Phe 115 120 125	626
25	ACC TGG GAA AAA CCC CCA GAA GAC CCT CCT GAT AGC AAG AAC ACA CTT Thr Trp Glu Lys Pro Pro Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu 130 135 140	674
30	GTG CTC TTT GGG GCA GGA TTC GGC GCA GTA ATA ACA GTC GTC GTC ATC Val Leu Phe Gly Ala Gly Phe Gly Ala Val Ile Thr Val Val Val Ile 145 150 155	722
35	GTT GTC ATC ATC AAA TGC TTC TGT AAG CAC GGT CTC ATC TAC CAT TTG Val Val Ile Ile Lys Cys Phe Cys Lys His Gly Leu Ile Tyr His Leu 160 165 170	770
40	CAA CTG ACC TCT TCT GCA AAG GAC TTC AGA AAC CTA GCA CTA CCC TGG Gln Leu Thr Ser Ser Ala Lys Asp Phe Arg Asn Leu Ala Leu Pro Trp 175 180 185 190	818
45	CTC TGC AAA CAC GGT TCT CTA GGT GAA GCC TCT GCA GTG ATT TGC AGA Leu Cys Lys His Gly Ser Leu Gly Glu Ala Ser Ala Val Ile Cys Arg 195 200 205	866
50	AGT ACT CAG ACG AAT GAA CCA CAG TAGTTCTGCT GTTTCTGAGG ACGTAGTTTA Ser Thr Gln Thr Asn Glu Pro Gln 210	920
55	GAGACTGAAT TCTTTGGAAA GGACATAGGG ACAGTTTGCA CATTTGCTTG CACATCACAC ACACACACAC ACACACACAC ACACACACAC ACACACACAC ACACACACAC ACACACACAC TCTCTCTCTC TCTCTCTCTC GATACCTTAG GATAGGGTTC TACCCTGTTG CTCAGTGACA AAGAATCACT CTGTGGCGGA GGCAGGCTTC AAGCTTGCAG CAATCCTCCT GCACCAGTTT CCTGAGTGCC AGACTTCCAG GTGTAAGCTA TGGCACTTAG CAGAACACTA GCTGAATCAA TGAAGACACT GAGGTTCCAA GAGGGAACCT GAATTATGAA GGTGAGTCAG AATCCAGATT TCCTGGCTCT ACCACTCTTA ACCTGTATCT GTTAGACCCC AAGCTCTGAG CTCATAGACA AGCTAATTTA AAATGCTTTT TAATAAGCAG AAGGCTCAGT TAGTACGGGG TTCAGGATAC TGCTTACTGG CAATATTTGA CTAGCCTCTA TTTTGTGTGT TTTTAAAGG CCTACTGACT	980 1040 1100 1160 1220 1280 1340 1400 1460

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GTAGTGTAAAT TTGTAGGAAA CATGTTGCTA TGTATACCCA TTGAGGGTA ATAAAAATGT 1520  
 TGGTAATTTT CAGCCAGCAC TTTCCAGGTA TTTCCCTTTT TATCCTTCAT 1570

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe  
 1 5 10 15  
 Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg Leu Ser  
 20 25 30  
 Gln Val Ser Ser Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly  
 35 40 45  
 Asn Pro Ser Ala Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly  
 50 55 60  
 Phe Pro Lys Pro Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro  
 65 70 75 80  
 Gly Ile Asn Thr Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr  
 85 90 95  
 Ile Ser Ser Gln Leu Asp Phe Asn Thr Thr Arg Asn His Thr Ile Lys  
 100 105 110  
 Cys Leu Ile Lys Tyr Gly Asp Ala His Val Ser Glu Asp Phe Thr Trp  
 115 120 125  
 Glu Lys Pro Pro Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu  
 130 135 140  
 Phe Gly Ala Gly Phe Gly Ala Val Ile Thr Val Val Val Ile Val Val  
 145 150 155 160  
 Ile Ile Lys Cys Phe Cys Lys His Gly Leu Ile Tyr His Leu Gln Leu  
 165 170 175  
 Thr Ser Ser Ala Lys Asp Phe Arg Asn Leu Ala Leu Pro Trp Leu Cys  
 180 185 190  
 Lys His Gly Ser Leu Gly Glu Ala Ser Ala Val Ile Cys Arg Ser Thr  
 195 200 205  
 Gln Thr Asn Glu Pro Gln  
 210

(2) INFORMATION FOR SEQ ID NO:12:

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 960280-52520280

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## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1261 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 194..1135

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AGNCCCNAGA TTATTTCTCC CTGTATAAGG GACGCCCAGG AGGCCTGGGG AGCGGACAAG 60  
 GCTCCTTTTA CTTTCTTCT TCTTCTATTT TTTTACGTT CTATTTTTTTT CTTTCATGTTT 120  
 CTGTGATCTT CGGGAATGCT GCTGTGCTTG TGTGTGTGGT CCCTGAGCGC CGAGGTGGAG 180  
 AGGCACTGGT GAC ATG TAT GTC ATC AAG ACA TGT GCA ACC TGC ACC ATG 229  
                   Met Tyr Val Ile Lys Thr Cys Ala Thr Cys Thr Met  
                   1                  5                  10  
 GGC TTG GCA ATC CTT ATC TTT GTG ACA GTC TTG CTG ATC TCA GAT GCT 277  
 Gly Leu Ala Ile Leu Ile Phe Val Thr Val Leu Leu Ile Ser Asp Ala  
                   15                  20                  25  
 GTT TCC GTG GAG ACG CAA GCT TAT TTC AAT GGG ACT GCA TAT CTG CCG 325  
 Val Ser Val Glu Thr Gln Ala Tyr Phe Asn Gly Thr Ala Tyr Leu Pro  
                   30                  35                  40  
 TGC CCA TTT ACA AAG GCT CAA AAC ATA AGC CTG AGT GAG CTG GTA GTA 373  
 Cys Pro Phe Thr Lys Ala Gln Asn Ile Ser Leu Ser Glu Leu Val Val  
                   45                  50                  55                  60  
 TTT TGG CAG GAC CAG CAA AAG TTG GTT CTG TAC GAG CAC TAT TTG GGC 421  
 Phe Trp Gln Asp Gln Gln Lys Leu Val Leu Tyr Glu His Tyr Leu Gly  
                   65                  70                  75  
 ACA GAG AAA CTT GAT AGT GTG AAT GCC AAG TAC CTG GGC CGC ACG AGC 469  
 Thr Glu Lys Leu Asp Ser Val Asn Ala Lys Tyr Leu Gly Arg Thr Ser  
                   80                  85                  90  
 TTT GAC AGG AAC AAC TGG ACT CTA CGA CTT CAC AAT GTT CAG ATC AAG 517  
 Phe Asp Arg Asn Asn Trp Thr Leu Arg Leu His Asn Val Gln Ile Lys  
                   95                  100                  105  
 GAC ATG GGC TCG TAT GAT TGT TTT ATA CAA AAA AAG CCA CCC ACA GGA 565  
 Asp Met Gly Ser Tyr Asp Cys Phe Ile Gln Lys Lys Pro Pro Thr Gly  
                   110                  115                  120  
 TCA ATT ATC CTC CAA CAG ACA TTA ACA GAA CTG TCA GTG ATC GCC AAC 613  
 Ser Ile Ile Leu Gln Gln Thr Leu Thr Glu Leu Ser Val Ile Ala Asn  
                   125                  130                  135                  140

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	TTC AGT GAA CCT GAA ATA AAA CTG GCT CAG AAT GTA ACA GGA AAT TCT	661
	Phe Ser Glu Pro Glu Ile Lys Leu Ala Gln Asn Val Thr Gly Asn Ser	
	145 150 155	
5	GGC ATA AAT TTG ACC TGC ACG TCT AAG CAA GGT CAC CCG AAA CCT AAG	709
	Gly Ile Asn Leu Thr Cys Thr Ser Lys Gln Gly His Pro Lys Pro Lys	
	160 165 170	
10	AAG ATG TAT TTT CTG ATA ACT AAT TCA ACT AAT GAG TAT GGT GAT AAC	757
	Lys Met Tyr Phe Leu Ile Thr Asn Ser Thr Asn Glu Tyr Gly Asp Asn	
	175 180 185	
15	ATG CAG ATA TCA CAA GAT AAT GTC ACA GAA CTG TTC AGT ATC TCC AAC	805
	Met Gln Ile Ser Gln Asp Asn Val Thr Glu Leu Phe Ser Ile Ser Asn	
	190 195 200	
20	AGC CTC TCT CTT TCA TTC CCG GAT GGT GTG TGG GAT ATG ACC GTT GTG	853
	Ser Leu Ser Leu Ser Phe Pro Asp Gly Val Trp His Met Thr Val Val	
	205 210 215 220	
25	TGT GTT CTG GAA ACG GAG TCA ATG AAG ATT TCC TCC AAA CCT CTC AAT	901
	Cys Val Leu Glu Thr Glu Ser Met Lys Ile Ser Ser Lys Pro Leu Asn	
	225 230 235	
30	TTC ACT CAA GAG TTT CCA TCT CCT CAA ACG TAT TGG AAG GAG ATT ACA	949
	Phe Thr Gln Glu Phe Pro Ser Pro Gln Thr Tyr Trp Lys Glu Ile Thr	
	240 245 250	
35	GCT TCA GTT ACT GTG GCC CTC CTC CTT GTG ATG CTG CTC ATC ATT GTA	997
	Ala Ser Val Thr Val Ala Leu Leu Leu Val Met Leu Leu Ile Ile Val	
	255 260 265	
40	TGT CAC AAG AAG CCG AAT CAG CCT AGC AGG CCC AGC AAC ACA GCC TCT	1045
	Cys His Lys Lys Pro Asn Gln Pro Ser Arg Pro Ser Asn Thr Ala Ser	
	270 275 280	
45	AAG TTA GAG CGG GAT AGT AAC GCT GAC AGA GAG ACT ATC AAC CTG AAG	1093
	Lys Leu Glu Arg Asp Ser Asn Ala Asp Arg Glu Thr Ile Asn Leu Lys	
	285 290 295 300	
50	GAA CTT GAA CCC CAA ATT GCT TCA GCA AAA CCA AAT GCA GAG	1135
	Glu Leu Glu Pro Gln Ile Ala Ser Ala Lys Pro Asn Ala Glu	
	305 310	
55	TGAAGGCAGT GAGAGCCTGA GGAAAGAGTT AAAAATTGCT TTGCCTGAAA TAAGAAGTGC	1195
	AGAGTTTCTC AGAATTCAAA AATGTTCTCA GCTGATTGGA ATTCTACAGT TGAATAATTA	1255
	AAGAAC	1261

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

5 Met Tyr Val Ile Lys Thr Cys Ala Thr Cys Thr Met Gly Leu Ala Ile  
 1 5 10 15  
 Leu Ile Phe Val Thr Val Leu Leu Ile Ser Asp Ala Val Ser Val Glu  
 20 25 30  
 10 Thr Gln Ala Tyr Phe Asn Gly Thr Ala Tyr Leu Pro Cys Pro Phe Thr  
 35 40 45  
 Lys Ala Gln Asn Ile Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp  
 50 55 60  
 15 Gln Gln Lys Leu Val Leu Tyr Glu His Tyr Leu Gly Thr Glu Lys Leu  
 65 70 75 80  
 20 Asp Ser Val Asn Ala Lys Tyr Leu Gly Arg Thr Ser Phe Asp Arg Asn  
 85 90 95  
 Asn Trp Thr Leu Arg Leu His Asn Val Gln Ile Lys Asp Met Gly Ser  
 100 105 110  
 25 Tyr Asp Cys Phe Ile Gln Lys Lys Pro Pro Thr Gly Ser Ile Ile Leu  
 115 120 125  
 Gln Gln Thr Leu Thr Glu Leu Ser Val Ile Ala Asn Phe Ser Glu Pro  
 130 135 140  
 30 Glu Ile Lys Leu Ala Gln Asn Val Thr Gly Asn Ser Gly Ile Asn Leu  
 145 150 155 160  
 35 Thr Cys Thr Ser Lys Gln Gly His Pro Lys Pro Lys Lys Met Tyr Phe  
 165 170 175  
 Leu Ile Thr Asn Ser Thr Asn Glu Tyr Gly Asp Asn Met Gln Ile Ser  
 180 185 190  
 40 Gln Asp Asn Val Thr Glu Leu Phe Ser Ile Ser Asn Ser Leu Ser Leu  
 195 200 205  
 Ser Phe Pro Asp Gly Val Trp His Met Thr Val Val Cys Val Leu Glu  
 210 215 220  
 45 Thr Glu Ser Met Lys Ile Ser Ser Lys Pro Leu Asn Phe Thr Gln Glu  
 225 230 235 240  
 50 Phe Pro Ser Pro Gln Thr Tyr Trp Lys Glu Ile Thr Ala Ser Val Thr  
 245 250 255  
 Val Ala Leu Leu Leu Val Met Leu Leu Ile Ile Val Cys His Lys Lys  
 260 265 270  
 55 Pro Asn Gln Pro Ser Arg Pro Ser Asn Thr Ala Ser Lys Leu Glu Arg  
 275 280 285  
 Asp Ser Asn Ala Asp Arg Glu Thr Ile Asn Leu Lys Glu Leu Glu Pro  
 290 295 300

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Gln Ile Ala Ser Ala Lys Pro Asn Ala Glu  
305 310

5 (2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 223 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 194..223

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AGNCCCNAGA TTATTTCTCC CTGTATAAGG GACGCCCAGG AGGCCTGGGG AGCGGACAAG 60  
25 GCTCCTTTTA CTTTCTTCT TCTTCTATTT TTTTACCTT CTATTTTTTTT CTTTCATGTTC 120  
CTGTGATCTT CGGGAATGCT GCTGTGCTTG TGTGTGTGGT CCCTGAGCGC CGAGGTGGAG 180  
AGGCACTGGT GAC ATG TAT GTC ATC AAG ACA TGT GCA ACC TGC 223  
Met Tyr Val Ile Lys Thr Cys Ala Thr Cys  
1 5 10

35 (2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

45 Met Tyr Val Ile Lys Thr Cys Ala Thr Cys  
1 5 10

(2) INFORMATION FOR SEQ ID NO:16:

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1716 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
55 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

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(A) NAME/KEY: CDS

(B) LOCATION: 249..1166.

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAGTTTATA CCTCAATAGA CTCTTACTAG TTTCTCTTTT TCAGGTTGTG AAACCTCAACC 60  
 TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG 120  
 TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTGTG GAGCCTAGGA 180  
 GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTT TCCAAAGCAT 240  
 15 CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC 290  
     Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu  
         1                    5                    10  
 AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT 338  
 20 Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg  
     15                    20                    25                    30  
 CTT TCA CAA GTG TCT TCA GAT GTT GAT GAA CAA CTG TCC AAG TCA GTG 386  
 25 Leu Ser Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val  
                     35                    40                    45  
 AAA GAT AAG GTA TTG CTG CCT TGC CGT TAC AAC TCT CCT CAT GAA GAT 434  
 Lys Asp Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp  
                     50                    55                    60  
 GAG TCT GAA GAC CGA ATC TAC TGG CAA AAA CAT GAC AAA GTG GTG CTG 482  
 30 Glu Ser Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu  
                     65                    70                    75  
 TCT GTC ATT GCT GGG AAA CTA AAA GTG TGG CCC GAG TAT AAG AAC CGG 530  
 35 Ser Val Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg  
         80                    85                    90  
 ACT TTA TAT GAC AAC ACT ACC TAC TCT CTT ATC ATC CTG GGC CTG GTC 578  
 40 Thr Leu Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val  
         95                    100                    105                    110  
 CTT TCA GAC CGG GGC ACA TAC AGC TGT GTC GTT CAA AAG AAG GAA AGA 626  
 45 Leu Ser Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg  
                     115                    120                    125  
 GGA ACG TAT GAA GTT AAA CAC TTG GCT TTA GTA AAG TTG TCC ATC AAA 674  
 Gly Thr Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys  
                     130                    135                    140  
 GCT GAC TTC TCT ACC CCC AAC ATA ACT GAG TCT GGA AAC CCA TCT GCA 722  
 Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro Ser Ala  
         145                    150                    155  
 GAC ACT AAA AGG ATT ACC TGC TTT GCT TCC GGG GGT TTC CCA AAG CCT 770  
 55 Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro Lys Pro  
         160                    165                    170

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CGC TTC TCT TGG TTG GAA AAT GGA AGA GAA TTA CCT GGC ATC AAT ACG 818  
 Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr  
 175 180 185 190

5 ACA ATT TCC CAG GAT CCT GAA TCT GAA TTG TAC ACC ATT AGT AGC CAA 866  
 Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln  
 195 200 205

10 CTA GAT TTC AAT ACG ACT CGC AAC CAC ACC ATT AAG TGT CTC ATT AAA 914  
 Leu Asp Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu Ile Lys  
 210 215 220

15 TAT GGA GAT GCT CAC GTG TCA GAG GAC TTC ACC TGG GAA AAA CCC CCA 962  
 Tyr Gly Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro  
 225 230 235

20 GAA GAC CCT CCT GAT AGC AAG AAC ACA CTT GTG CTC TTT GGG GCA GGA 1010  
 Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly  
 240 245 250

TTC GGC GCA GTA ATA ACA GTC GTC GTC ATC GTT GTC ATC ATC AAA TGC 1058  
 Phe Gly Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys  
 255 260 265 270

25 TTC TGT AAG CAC AGA AGC TGT TTC AGA AGA AAT GAG GCA AGC AGA GAA 1106  
 Phe Cys Lys His Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser Arg Glu  
 275 280 285

30 ACA AAC AAC AGC CTT ACC TTC GGG CCT GAA GAA GCA TTA GCT GAA CAG 1154  
 Thr Asn Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln  
 290 295 300

35 ACC GTC TTC CTT TAGTTCTTCT CTGTCCATGT GGGATACATG GTATTATGTG 1206  
 Thr Val Phe Leu  
 305

GCTCATGAGG TACAATCTTT CTTTCAGCAC CGTGCTAGCT GATCTTTCGG ACAACTTGAC 1266

40 ACAAGATAGA GTTAACTGGG AAGAGAAAGC CTTGAATGAG GATTTCTTTC CATCAGGAAG 1326

CTACGGGCAA GTTTGCTGGG CCTTTGATTG CTTGATGACT GAAGTGGAAA GGCTGAGCCC 1386

ACTGTGGGTG GTGCTAGCCC TGGGCAGGGG CAGGTGACCC TGGGTGGTAT AAGAAAAAGA 1446

45 GCTGTCACTA AAAGGAGAGG TGCCTAGTCT TACTGCAACT TGATATGTCA TGTTTGGTTG 1506

GTGTCTGTGG GAGGCCTGCC CTTTTCTGAA GAGAAGTGGT GGGAGAGTGG ATGGGGTGGG 1566

50 GGCAGAGGAA AAGTGGGGGA GAGGGCCTGG GAGGAGAGGA GGGAGGGGGA CGGGGTGGGG 1626

GTGGGGAAAA CTATGGTTGG GATGTAAAAA CGGATAATAA TATAAATATT AAATAAAAAG 1686

AGAGTATTGA GCAAAAAAAA AAAAAAAA 1716

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 306 amino acids

08702525-083095

(E) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe  
 1 5 10 15  
 Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg Leu Ser  
 20 25 30  
 Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val Lys Asp  
 35 40 45  
 Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp Glu Ser  
 50 55 60  
 Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu Ser Val  
 65 70 75 80  
 Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg Thr Leu  
 85 90 95  
 Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val Leu Ser  
 100 105 110  
 Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg Gly Thr  
 115 120 125  
 Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys Ala Asp  
 130 135 140  
 Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro Ser Ala Asp Thr  
 145 150 155 160  
 Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro Lys Pro Arg Phe  
 165 170 175  
 Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr Thr Ile  
 180 185 190  
 Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln Leu Asp  
 195 200 205  
 Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu Ile Lys Tyr Gly  
 210 215 220  
 Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro Glu Asp  
 225 230 235 240  
 Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly Phe Gly  
 245 250 255  
 Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys Phe Cys  
 260 265 270

08702525-0820280

Lys His Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser Arg Glu Thr Asn  
 275 280 285

Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln Thr Val  
 290 295 300

Phe Leu  
 305

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1491 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 318..1181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCAAAGAAAA AGTGATTTGT CATTGCTTTA TAGACTGTAA GAAGAGAACA TCTCAGAAGT 60  
 GGAGTCTTAC CCTGAAATCA AAGGATTTAA AGAAAAAGTG GAATTTTCTC TCAGCAAGCT 120  
 GTGAAACTAA ATCCACAACC TTTGGAGACC CAGGAACACC CTCCAATCTC TGTGTGTTTT 180  
 GTAAACATCA CTGGAGGGTC TTCTACGTGA GCAATTGGAT TGTCATCAGC CCTGCCTGTT 240  
 TTGCACCTGG GAAGTGCCCT GGTCTTACTT GGGTCCAAAT TGTGCGCTTT CACTTTTGAC 300  
 CCTAAGCATC TGAAGCC ATG GGC CAC ACA CGG AGG CAG GGA ACA TCA CCA 350  
 Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro  
 1 5 10  
 TCC AAG TGT CCA TAC CTG AAT TTC TTT CAG CTC TTG GTG CTG GCT GGT 398  
 Ser Lys Cys Pro Tyr Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly  
 15 20 25  
 CTT TCT CAC TTC TGT TCA GGT GTT ATC CAC GTG ACC AAG GAA GTG AAA 446  
 Leu Ser His Phe Cys Ser Gly Val Ile His Val Thr Lys Glu Val Lys  
 30 35 40  
 GAA GTG GCA ACG CTG TCC TGT GGT CAC AAT GTT TCT GTT GAA GAG CTG 494  
 Glu Val Ala Thr Leu Ser Cys Gly His Asn Val Ser Val Glu Glu Leu  
 45 50 55  
 GCA CAA ACT CGC ATC TAC TGG CAA AAG GAG AAG AAA ATG GTG CTG ACT 542  
 Ala Gln Thr Arg Ile Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr  
 60 65 70 75

08702525-083096

Subal

	ATG	ATG	TCT	GGG	GAC	ATG	AAT	ATA	TGG	CCC	GAG	TAC	AAG	AAC	CGG	ACC	
	Met	Met	Ser	Gly	Asp	Met	Asn	Ile	Trp	Pro	Glu	Tyr	Lys	Asn	Arg	Thr	
				80						85					90		590
5	ATC	TTT	GAT	ATC	ACT	AAT	AAC	CTC	TCC	ATT	GTG	ATC	CTG	GCT	CTG	CGC	638
	Ile	Phe	Asp	Ile	Thr	Asn	Asn	Leu	Ser	Ile	Val	Ile	Leu	Ala	Leu	Arg	
				95					100					105			
10	CCA	TCT	GAC	GAG	GGC	ACA	TAC	GAG	TGT	GTT	GTT	CTG	AAG	TAT	GAA	AAA	686
	Pro	Ser	Asp	Glu	Gly	Thr	Tyr	Glu	Cys	Val	Val	Leu	Lys	Tyr	Glu	Lys	
				110				115					120				
15	GAC	GCT	TTC	AAG	CGG	GAA	CAC	CTG	GCT	GAA	GTG	ACG	TTA	TCA	GTC	AAA	734
	Asp	Ala	Phe	Lys	Arg	Glu	His	Leu	Ala	Glu	Val	Thr	Leu	Ser	Val	Lys	
				125			130					135					
20	GCT	GAC	TTC	CCT	ACA	CCT	AGT	ATA	TCT	GAC	TTT	GAA	ATT	CCA	ACT	TCT	782
	Ala	Asp	Phe	Pro	Thr	Pro	Ser	Ile	Ser	Asp	Phe	Glu	Ile	Pro	Thr	Ser	
						145				150					155		
25	AAT	ATT	AGA	AGG	ATA	ATT	TGC	TCA	ACC	TCT	GGA	GGT	TTT	CCA	GAG	CCT	830
	Asn	Ile	Arg	Arg	Ile	Ile	Cys	Ser	Thr	Ser	Gly	Gly	Phe	Pro	Glu	Pro	
					160					165					170		
30	CAC	CTC	TCC	TGG	TTG	GAA	AAT	GGA	GAA	GAA	TTA	AAT	GCC	ATC	AAC	ACA	878
	His	Leu	Ser	Trp	Leu	Glu	Asn	Gly	Glu	Glu	Leu	Asn	Ala	Ile	Asn	Thr	
				175				180					185				
35	ACA	GTT	TCC	CAA	GAT	CCT	GAA	ACT	GAG	CTC	TAT	GCT	GTT	AGC	AGC	AAA	926
	Thr	Val	Ser	Gln	Asp	Pro	Glu	Thr	Glu	Leu	Tyr	Ala	Val	Ser	Ser	Lys	
				190				195					200				
40	CTG	GAT	TTC	AAT	ATG	ACA	ACC	AAC	CAC	AGC	TTC	ATG	TGT	CTC	ATC	AAG	974
	Leu	Asp	Phe	Asn	Met	Thr	Thr	Asn	His	Ser	Phe	Met	Cys	Leu	Ile	Lys	
		205					210				215						
45	TAT	GGA	CAT	TTA	AGA	GTG	AAT	CAG	ACC	TTC	AAC	TGG	AAT	ACA	ACC	AAG	1022
	Tyr	Gly	His	Leu	Arg	Val	Asn	Gln	Thr	Phe	Asn	Trp	Asn	Thr	Thr	Lys	
		220				225				230					235		
50	CAA	GAG	CAT	TTT	CCT	GAT	AAC	CTG	CTC	CCA	TCC	TGG	GCC	ATT	ACC	TTA	1070
	Gln	Glu	His	Phe	Pro	Asp	Asn	Leu	Leu	Pro	Ser	Trp	Ala	Ile	Thr		



AAGCTGAACA GTTACAAGAT GGCTGGCATC CCTCTCCTTT CTCCCCATAT GCAATTTGCT 1401  
 TAATGTAACC TCTTCTTTTG CCATGTTTCC ATTCTGCCAT CTTGAATTGT CTTGTCAGCC 1461  
 AATTCATTAT CTATTAAACA CTAATTTGAG 1491

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr  
 1 5 10 15  
 Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys  
 20 25 30  
 Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu  
 35 40 45  
 Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile  
 50 55 60  
 Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp  
 65 70 75 80  
 Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr  
 85 90 95  
 Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly  
 100 105 110  
 Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg  
 115 120 125  
 Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr  
 130 135 140  
 Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile  
 145 150 155 160  
 Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu  
 165 170 175  
 Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp  
 180 185 190  
 Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met  
 195 200 205

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 966990-52520280

Subal

Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg  
210 215 220

Val Asn Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro  
225 230 235 240

Asp Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly  
245 250 255

Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg  
260 265 270

Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val  
275 280 285

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1151 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 99..1025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

35 GGAGCAAGCA GACGCGTAAG AGTGGCTCCT GTAGGCAGCA CGGACTTGAA CAACCAGACT 60  
CCTGTAGACG TGTTCCAGAA CTTACGGAAG CACCCACG ATG GAC CCC AGA TGC 113  
Met Asp Pro Arg Cys  
1 5  
40 ACC ATG GGC TTG GCA ATC CTT ATC TTT GTG ACA GTC TTG CTG ATC TCA 161  
Thr Met Gly Leu Ala Ile Leu Ile Phe Val Thr Val Leu Leu Ile Ser  
10 15 20  
45 GAT GCT GTT TCC GTG GAG ACG CAA GCT TAT TTC AAT GGG ACT GCA TAT 209  
Asp Ala Val Ser Val Glu Thr Gln Ala Tyr Phe Asn Gly Thr Ala Tyr  
25 30 35  
50 CTG CCG TGC CCA TTT ACA AAG GCT CAA AAC ATA AGC CTG AGT GAG CTG 257  
Leu Pro Cys Pro Phe Thr Lys Ala Gln Asn Ile Ser Leu Ser Glu Leu  
40 45 50  
55 GTA GTA TTT TGG CAG GAC CAG CAA AAG TTG GTT CTG TAC GAG CAC TAT 305  
Val Val Phe Trp Gln Asp Gln Gln Lys Leu Val Leu Tyr Glu His Tyr  
55 60 65  
TTG GGC ACA GAG AAA CTT GAT AGT GTG AAT GCC AAG TAC CTG GGC CGC 353  
Leu Gly Thr Glu Lys Leu Asp Ser Val Asn Ala Lys Tyr Leu Gly Arg  
70 75 80 85

960E30 52520/280

806  
a1

ACG AGC TTT GAC AGG AAC AAC TGG ACT CTA CGA CTT CAC AAT GTT CAG 401  
 Thr Ser Phe Asp Arg Asn Asn Trp Thr Leu Arg Leu His Asn Val Gln  
 90 95 100  
 5 ATC AAG GAC ATG GGC TCG TAT GAT TGT TTT ATA CAA AAA AAG CCA CCC 449  
 Ile Lys Asp Met Gly Ser Tyr Asp Cys Phe Ile Gln Lys Lys Pro Pro  
 105 110 115  
 10 ACA GGA TCA ATT ATC CTC CAA CAG ACA TTA ACA GAA CTG TCA GTG ATC 497  
 Thr Gly Ser Ile Ile Leu Gln Gln Thr Leu Thr Glu Leu Ser Val Ile  
 120 125 130  
 15 GCC AAC TTC AGT GAA CCT GAA ATA AAA CTG GCT CAG AAT GTA ACA GGA 545  
 Ala Asn Phe Ser Glu Pro Glu Ile Lys Leu Ala Gln Asn Val Thr Gly  
 135 140 145  
 20 AAT TCT GGC ATA AAT TTG ACC TGC ACG TCT AAG CAA GGT CAC CCG AAA 593  
 Asn Ser Gly Ile Asn Leu Thr Cys Thr Ser Lys Gln Gly His Pro Lys  
 150 155 160 165  
 25 CCT AAG AAG ATG TAT TTT CTG ATA ACT AAT TCA ACT AAT GAG TAT GGT 641  
 Pro Lys Lys Met Tyr Phe Leu Ile Thr Asn Ser Thr Asn Glu Tyr Gly  
 170 175 180  
 GAT AAC ATG CAG ATA TCA CAA GAT AAT GTC ACA GAA CTG TTC AGT ATC 689  
 Asp Asn Met Gln Ile Ser Gln Asp Asn Val Thr Glu Leu Phe Ser Ile  
 185 190 195  
 30 TCC AAC AGC CTC TCT CTT TCA TTC CCG GAT GGT GTG TGG CAT ATG ACC 737  
 Ser Asn Ser Leu Ser Leu Ser Phe Pro Asp Gly Val Trp His Met Thr  
 200 205 210  
 35 GTT GTG TGT GTT CTG GAA ACG GAG TCA ATG AAG ATT TCC TCC AAA CCT 785  
 Val Val Cys Val Leu Glu Thr Glu Ser Met Lys Ile Ser Ser Lys Pro  
 215 220 225  
 CTC AAT TTC ACT CAA GAG TTT CCA TCT CCT CAA ACG TAT TGG AAG GAG 833  
 Leu Asn Phe Thr Gln Glu Phe Pro Ser Pro Gln Thr Tyr Trp Lys Glu  
 230 235 240 245  
 40 ATT ACA GCT TCA GTT ACT GTG GCC CTC CTC CTT GTG ATG CTG CTC ATC 881  
 Ile Thr Ala Ser Val Thr Val Ala Leu Leu Leu Val Met Leu Leu Ile  
 250 255 260  
 45 ATT GTA TGT CAC AAG AAG CCG AAT CAG CCT AGC AGG CCC AGC AAC ACA 929  
 Ile Val Cys His Lys Lys Pro Asn Gln Pro Ser Arg Pro Ser Asn Thr  
 265 270 275  
 50 GCC TCT AAG TTA GAG CGG GAT AGT AAC GCT GAC AGA GAG ACT ATC AAC 977  
 Ala Ser Lys Leu Glu Arg Asp Ser Asn Ala Asp Arg Glu Thr Ile Asn  
 280 285 290  
 55 CTG AAG GAA CTT GAA CCC CAA ATT GCT TCA GCA AAA CCA AAT GCA GAG 1025  
 Leu Lys Glu Leu Glu Pro Gln Ile Ala Ser Ala Lys Pro Asn Ala Glu  
 295 300 305  
 TGAAGGCAGT GAGAGCCTGA GGAAAGAGTT AAAAATTGCT TTGCCTGAAA TAAGAAGTGC 1085

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Sub as

AGAGTTTCTC AGAATTCAAA AATGTTCTCA GCTGATTGGA ATTCTACAGT TGAATAATTA 1145

AAGAAC 1151

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 309 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Asp Pro Arg Cys Thr Met Gly Leu Ala Ile Leu Ile Phe Val Thr  
1 5 10 15

20 Val Leu Leu Ile Ser Asp Ala Val Ser Val Glu Thr Gln Ala Tyr Phe  
20 25 30

Asn Gly Thr Ala Tyr Leu Pro Cys Pro Phe Thr Lys Ala Gln Asn Ile  
35 40 45

Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp Gln Gln Lys Leu Val  
50 55 60

30      Leu Tyr Glu His Tyr Leu Gly Thr Glu Lys Leu Asp Ser Val Asn Ala  
          65                         70                         75                         80

Lys Tyr Leu Gly Arg Thr Ser Phe Asp Arg Asn Asn Trp Thr Leu Arg  
85 90 95

35    Leu His Asn Val Gln Ile Lys Asp Met Gly Ser Tyr Asp Cys Phe Ile  
                    100                    105                    110

Gln Lys Lys Pro Pro Thr Gly Ser Ile Ile Leu Gln Gln Thr Leu Thr  
115 120 125

Glu Leu Ser Val Ile Ala Asn Phe Ser Glu Pro Glu Ile Lys Leu Ala  
130 135 140

45      Gln Asn Val Thr Gly Asn Ser Gly Ile Asn Leu Thr Cys Thr Ser Lys  
         145                150                155                160

Gln Gly His Pro Lys Pro Lys Lys Met Tyr Phe Leu Ile Thr Asn Ser  
165 170 175

50 Thr Asn Glu Tyr Gly Asp Asn Met Gln Ile Ser Gln Asp Asn Val Thr  
180 185 190

Glu Leu Phe Ser Ile Ser Asn Ser Leu Ser Leu Ser Phe Pro Asp Gly  
195 200 205

55 Val Trp His Met Thr Val Val Cys Val Leu Glu Thr Glu Ser Met Lys  
210 215 220

Ile Ser Ser Lys Pro Leu Asn Phe Thr Gln Glu Phe Pro Ser Pro Gln  
225 230 235 240

Thr Tyr Trp Lys Glu Ile Thr Ala Ser Val Thr Val Ala Leu Leu Leu  
245 250 255

Val Met Leu Leu Ile Ile Val Cys His Lys Lys Pro Asn Gln Pro Ser  
260 265 270

Arg Pro Ser Asn Thr Ala Ser Lys Leu Glu Arg Asp Ser Asn Ala Asp  
275 280 285

Arg Glu Thr Ile Asn Leu Lys Glu Leu Glu Pro Gln Ile Ala Ser Ala  
290 295 300

Lys Pro Asn Ala Glu  
305

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 107..1093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CACAGGGTGA AAGCTTTGCT TCTCTGCTGC TGTAACAGGG ACTAGCACAG ACACACGGAT 60

GAGTGGGGTC ATTTCCAGAT ATTAGGTCAC AGCAGAAGCA GCCAAA ATG GAT CCC 115  
Met Asp Pro  
1

CAG TGC ACT ATG GGA CTG AGT AAC ATT CTC TTT GTG ATG GCC TTC CTG 163  
Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu  
5 10 15

CTC TCT GGT GCT GCT CCT CTG AAG ATT CAA GCT TAT TTC AAT GAG ACT 211  
Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr  
20 25 30 35

GCA GAC CTG CCA TGC CAA TTT GCA AAC TCT CAA AAC CAA AGC CTG AGT 259  
Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser  
40 45 50

GAG CTA GTA GTA TTT TGG CAG GAC CAG GAA AAC TTG GTT CTG AAT GAG 307  
Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu  
55 60 65

08702555 083095 560280 525220/80

Sub 35  
al

	GTA TAC TTA GGC AAA GAG AAA TTT GAC AGT GTT CAT TCC AAG TAT ATG Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met	355
	70 75 80	
5	GGC CGC ACA AGT TTT GAT TCG GAC AGT TGG ACC CTG AGA CTT CAC AAT Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn	403
	85 90 95	
10	CTT CAG ATC AAG GAC AAG GGC TTG TAT CAA TGT ATC ATC CAT CAC AAA Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys	451
	100 105 110 115	
15	AAG CCC ACA GGA ATG ATT CGC ATC CAC CAG ATG AAT TCT GAA CTG TCA Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser	499
	120 125 130	
20	GTG CTT GCT AAC TTC AGT CAA CCT GAA ATA GTA CCA ATT TCT AAT ATA Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile	547
	135 140 145	
25	ACA GAA AAT GTG TAC ATA AAT TTG ACC TGC TCA TCT ATA CAC GGT TAC Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr	595
	150 155 160	
30	CCA GAA CCT AAG AAG ATG AGT GTT TTG CTA AGA ACC AAG AAT TCA ACT Pro Glu Pro Lys Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr	643
	165 170 175	
35	ATC GAG TAT GAT GGT ATT ATG CAG AAA TCT CAA GAT AAT GTC ACA GAA Ile Glu Tyr Asp Gly Ile Met Gln Lys Ser Gln Asp Asn Val Thr Glu	691
	180 185 190 195	
40	CTG TAC GAC GTT TCC ATC AGC TTG TCT GTT TCA TTC CCT GAT GTT ACG Leu Tyr Asp Val Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr	739
	200 205 210	
45	AGC AAT ATG ACC ATC TTC TGT ATT CTG GAA ACT GAC AAG ACG CGG CTT Ser Asn Met Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu	787
	215 220 225	
50	TTA TCT TCA CCT TTC TCT ATA GAG CTT GAG GAC CCT CAG CCT CCC CCA Leu Ser Ser Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro	835
	230 235 240	
55	GAC CAC ATT CCT TGG ATT ACA GCT GTA CTT CCA ACA GTT ATT ATA TGT Asp His Ile Pro Trp Ile Thr Ala Val Leu Pro Thr Val Ile Ile Cys	883
	245 250 255	
60	GTG ATG GTT TTC TGT CTA ATT CTA TGG AAA TGG AAG AAG AAG AAG CGG Val Met Val Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys Lys Lys Arg	931
	260 265 270 275	
65	CCT CGC AAC TCT TAT AAA TGT GGA ACC AAC ACA ATG GAG AGG GAA GAG Pro Arg Asn Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu Arg Glu Glu	979
	280 285 290	
70	AGT GAA CAG ACC AAG AAA AGA GAA AAA ATC CAT ATA CCT GAA AGA TCT Ser Glu Gln Thr Lys Lys Arg Glu Lys Ile His Ile Pro Glu Arg Ser	1027
	295 300 305	

03/02/95 08:30:06

Sub  
al

GAT GAA GCC CAG CGT GTT TTT AAA AGT TCG AAG ACA TCT TCA TGC GAC 1075  
 Asp Glu Ala Gln Arg Val Phe Lys Ser Ser Lys Thr Ser Ser Cys Asp  
 310 315 320

5 AAA AGT GAT ACA TGT TTT TAATTAAAGA GTAAAGCCCA AAAAAAA 1120  
 Lys Ser Asp Thr Cys Phe  
 325

10 (2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 329 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Asp Pro Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met  
 1 5 10 15

25 Ala Phe Leu Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe  
 20 25 30

Asn Glu Thr Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln  
 35 40 45

Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val  
 50 55 60

Leu Asn Glu Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser  
 65 70 75 80

Lys Tyr Met Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg  
 85 90 95

40 Leu His Asn Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile  
 100 105 110

His His Lys Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser  
 115 120 125

45 Glu Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile  
 130 135 140

50 Ser Asn Ile Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile  
 145 150 155 160

His Gly Tyr Pro Glu Pro Lys Lys Met Ser Val Leu Leu Arg Thr Lys  
 165 170 175

55 Asn Ser Thr Ile Glu Tyr Asp Gly Ile Met Gln Lys Ser Gln Asp Asn  
 180 185 190

Val Thr Glu Leu Tyr Asp Val Ser Ile Ser Leu Ser Val Ser Phe Pro  
 195 200 205

08706525-083006  
 Sub  
 al

Asp Val Thr Ser Asn Met Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys  
210 215 220

5 Thr Arg Leu Leu Ser Ser Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln  
225 230 235 240

Pro Pro Pro Asp His Ile Pro Trp Ile Thr Ala Val Leu Pro Thr Val  
245 250 255

Ile Ile Cys Val Met Val Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys  
260 265 270

15 Lys Lys Arg Pro Arg Asn Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu  
275 280 285

Arg Glu Glu Ser Glu Gln Thr Lys Lys Arg Glu Lys Ile His Ile Pro  
290 295 300

20    Glu Arg Ser Asp Glu Ala Gln Arg Val Phe Lys Ser Ser Lys Thr Ser  
       305                      310                      315                      320

Ser Cys Asp Lys Ser Asp Thr Cys Phe  
325

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1161 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 148..1134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AGGAGCCTTA GGAGGTACGG GGAGCTCGCA AATACTCCTT TTGGTTTATT CTTACCACCT 60

TGCTTCTGTG TTCCTTGGGA ATGCTGCTGT GCTTATGCAT CTGGTCTCTT TTTGGAGCTA 120

CAGTGGACAG GCATTTGTGA CAGCACT ATG GAT CCC CAG TGC ACT ATG GGA  
Met Asp Pro Gln Cys Thr Met Gly 171

CTG AGT AAC ATT CTC TTT GTG ATG GCC TTC CTG CTC TCT GGT GCT GCT 219  
Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu Leu Ser Gly Ala Ala  
10 15 20

CCT CTG AAG ATT CAA GCT TAT TTC AAT GAG ACT GCA GAC CTG CCA TGC 267  
Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu Pro Cys  
25 30 35 40

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Sub a1



	CAA	TTT	GCA	AAC	TCT	CAA	AAC	CAA	AGC	CTG	AGT	GAG	CTA	GTA	GTA	TTT	315
	Gln	Phe	Ala	Asn	Ser	Gln	Asn	Gln	Ser	Leu	Ser	Glu	Leu	Val	Val	Phe	
					45					50						55	
5	TGG	CAG	GAC	CAG	GAA	AAC	TTG	GTT	CTG	AAT	GAG	GTA	TAC	TTA	GGC	AAA	363
	Trp	Gln	Asp	Gln	Glu	Asn	Leu	Val	Leu	Asn	Glu	Val	Tyr	Leu	Gly	Lys	
				60					65					70			
10	GAG	AAA	TTT	GAC	AGT	GTT	CAT	TCC	AAG	TAT	ATG	GGC	CGC	ACA	AGT	TTT	411
	Glu	Lys	Phe	Asp	Ser	Val	His	Ser	Lys	Tyr	Met	Gly	Arg	Thr	Ser	Phe	
			75					80					85				
15	GAT	TCG	GAC	AGT	TGG	ACC	CTG	AGA	CTT	CAC	AAT	CTT	CAG	ATC	AAG	GAC	459
	Asp	Ser	Asp	Ser	Trp	Thr	Leu	Arg	Leu	His	Asn	Leu	Gln	Ile	Lys	Asp	
		90					95					100					
20	AAG	GGC	TTG	TAT	CAA	TGT	ATC	ATC	CAT	CAC	AAA	AAG	CCC	ACA	GGA	ATG	507
	Lys	Gly	Leu	Tyr	Gln	Cys	Ile	Ile	His	His	Lys	Lys	Pro	Thr	Gly	Met	
	105					110					115					120	
25	ATT	CGC	ATC	CAC	CAG	ATG	AAT	TCT	GAA	CTG	TCA	GTG	CTT	GCT	AAC	TTC	555
	Ile	Arg	Ile	His	Gln	Met	Asn	Ser	Glu	Leu	Ser	Val	Leu	Ala	Asn	Phe	
					125					130					135		
30	AGT	CAA	CCT	GAA	ATA	GTA	CCA	ATT	TCT	AAT	ATA	ACA	GAA	AAT	GTG	TAC	603
	Ser	Gln	Pro	Glu	Ile	Val	Pro	Ile	Ser	Asn	Ile	Thr	Glu	Asn	Val	Tyr	
				140					145					150			
35	ATA	AAT	TTG	ACC	TGC	TCA	TCT	ATA	CAC	GGT	TAC	CCA	GAA	CCT	AAG	AAG	651
	Ile	Asn	Leu	Thr	Cys	Ser	Ser	Ile	His	Gly	Tyr	Pro	Glu	Pro	Lys	Lys	
			155					160					165				
40	ATG	AGT	GTT	TTG	CTA	AGA	ACC	AAG	AAT	TCA	ACT	ATC	GAG	TAT	GAT	GGT	699
	Met	Ser	Val	Leu	Leu	Arg	Thr	Lys	Asn	Ser	Thr	Ile	Glu	Tyr	Asp	Gly	
		170					175					180					
45	ATT	ATG	CAG	AAA	TCT	CAA	GAT	AAT	GTC	ACA	GAA	CTG	TAC	GAC	GTT	TCC	747
	Ile	Met	Gln	Lys	Ser	Gln	Asp	Asn	Val	Thr	Glu	Leu	Tyr	Asp	Val	Ser	
	185					190					195					200	
50	ATC	AGC	TTG	TCT	GTT	TCA	TTC	CCT	GAT	GTT	ACG	AGC	AAT	ATG	ACC	ATC	795
	Ile	Ser	Leu	Ser	Val	Ser	Phe	Pro	Asp	Val	Thr	Ser	Asn	Met	Thr	Ile	
					205					210					215		
55	TTC	TGT	ATT	CTG	GAA	ACT	GAC	AAG	ACG	CGG	CTT	TTA	TCT	TCA	CCT	TTC	843
	Phe	Cys	Ile	Leu	Glu	Thr	Asp	Lys	Thr	Arg	Leu	Leu	Ser	Ser	Pro	Phe	
				220					225					230			
60	TCT	ATA	GAG	CTT	GAG	GAC	CCT	CAG	CCT	CCC	CCA	GAC	CAC	ATT	CCT	TGG	891
	Ser	Ile	Glu	Leu	Glu	Asp	Pro	Gln	Pro	Pro	Pro	Asp	His	Ile	Pro	Trp	
			235					240					245				
65	ATT	ACA	GCT	GTA	CTT	CCA	ACA	GTT	ATT	ATA	TGT	GTG	ATG	GTT	TTC	TGT	939
	Ile	Thr	Ala	Val	Leu	Pro	Thr	Val	Ile	Ile	Cys	Val	Met	Val	Phe	Cys	
		250					255					260					
70	CTA	ATT	CTA	TGG	AAA	TGG	AAG	AAG	AAG	AAG	CGG	CCT	CGC	AAC	TCT	TAT	987
	Leu	Ile	Leu	Trp	Lys	Trp	Lys	Lys	Lys	Lys	Arg	Pro	Arg	Asn	Ser	Tyr	
	265					270					275					280	

550580-52520280

Sub  
at

AAA TGT GGA ACC AAC ACA ATG GAG AGG GAA GAG AGT GAA CAG ACC AAG 1035  
 Lys Cys Gly Thr Asn Thr Met Glu Arg Glu Glu Ser Glu Gln Thr Lys  
 285 290 295

AAA AGA GAA AAA ATC CAT ATA CCT GAA AGA TCT GAT GAA GCC CAG CGT 1083  
 Lys Arg Glu Lys Ile His Ile Pro Glu Arg Ser Asp Glu Ala Gln Arg  
 300 305 310

GTT TTT AAA AGT TCG AAG ACA TCT TCA TGC GAC AAA AGT GAT ACA TGT 1131  
 Val Phe Lys Ser Ser Lys Thr Ser Ser Cys Asp Lys Ser Asp Thr Cys  
 315 320 325

TTT TAATTAAAGA GTAAAGCCCA AAAAAA 1161  
 Phe

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 629 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..96

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AGA AGC TGT TTC AGA AGA AAT GAG GCA AGC AGA GAA ACA AAC AAC AGC 48  
 Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser Arg Glu Thr Asn Asn Ser  
 1 5 10 15

CTT ACC TTC GGG CCT GAA GAA GCA TTA GCT GAA CAG ACC GTC TTC CTT 96  
 Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln Thr Val Phe Leu  
 20 25 30

TAGTTCTTCT CTGTCCATGT GGGATACATG GTATTATGTG GCTCATGAGG TACAATCTTT 156

CTTTCAGCAC CGTGCTAGCT GATCTTTCGG ACAACTTGAC ACAAGATAGA GTTAAGTGGG 216

AAGAGAAAGC CTTGAATGAG GATTTCTTTC CATCAGGAAG CTACGGGCAA GTTTGCTGGG 276

CCTTTGATTG CTTGATGACT GAAGTGGAAA GGCTGAGCCC ACTGTGGGTG GTGCTAGAAA 336

TGGGCAGGGG CAGGTGACCC TGGGTGGTAT AAGAAAAAGA GCTGTCACTA AAAGGAGAGG 396

TGCCTAGTCT TACTGCAACT TGATATGTCA TGTTTGGTTG GTGTCTGTGG GAGGCCTGCC 456

CTTTTCTGAA GAGAAGTGGT GGGAGAGTGG ATGGGGTGGG GGCAGAGGAA AAGTGGGGGA 516

GAGGGCCTGG GAGGAGAGGA GGGAGGGGGA CGGGGTGGGG GTGGGGAAAA CTATGGTTGG 576

960380-52520/80

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35

GATGTAAAA CGGATAATAA TATAAATATT AAATAAAAAG AGAGTATTGA GCA

629

## 5 (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

15 Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser Arg Glu Thr Asn Asn Ser  
1 5 10 15  
20 Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln Thr Val Phe Leu  
20 25 30

## (2) INFORMATION FOR SEQ ID NO:27:

## 25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 379 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30 *Sub* (ii) MOLECULE TYPE: cDNA

## 35 (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..69

## 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

45 TGC TTT GCC CCA AGA TGC AGA GAG AGA AGG AGG AAT GAG AGA TTG AGA 48  
Cys Phe Ala Pro Arg Cys Arg Glu Arg Arg Arg Asn Glu Arg Leu Arg  
1 5 10 15

AGG GAA AGT GTA CGC CCT GTA TAACAGTGTG CGCAGAAGCA AGGGGCTGAA 99  
Arg Glu Ser Val Arg Pro Val  
20

50 AAGATCTGAA GGTAGCCTCC GTCATCTCTT CTGGGATACA TGGATCGTGG GGATCATGAG 159

GCATTCTTCC CTTAACAAAT TTAAGCTGTT TTACCCACTA CCTCACCTTC TTAAAAACCT 219

CTTTCAGATT AAGCTGAACA GTTACAAGAT GGCTGGCATC CCTCTCCTTT CTCCCCATAT 279

55 GCAATTTGCT TAATGTAACC TCTTCTTTTG CCATGTTTCC ATTCTGCCAT CTTGAATTGT 339

CTTGTCAGCC AATTCATTAT CTATTAAACA CTAATTTGAG 379

## (2) INFORMATION FOR SEQ ID NO:28:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Cys Phe Ala Pro Arg Cys Arg Glu Arg Arg Arg Asn Glu Arg Leu Arg  
 1 5 10 15  
 Arg Glu Ser Val Arg Pro Val  
 20

## (2) INFORMATION FOR SEQ ID NO:29:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..135

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CAC AAG AAG CCG AAT CAG CCT AGC AGG CCC AGC AAC ACA GCC TCT AAG 48  
 His Lys Lys Pro Asn Gln Pro Ser Arg Pro Ser Asn Thr Ala Ser Lys  
 1 5 10 15  
 TTA GAG CGG GAT AGT AAC GCT GAC AGA GAG ACT ATC AAC CTG AAG GAA 96  
 Leu Glu Arg Asp Ser Asn Ala Asp Arg Glu Thr Ile Asn Leu Lys Glu  
 20 25 30  
 CTT GAA CCC CAA ATT GCT TCA GCA AAA CCA AAT GCA GAG TGAAGGCAGT 145  
 Leu Glu Pro Gln Ile Ala Ser Ala Lys Pro Asn Ala Glu  
 35 40 45  
 GAGAGCCTGA GGAAAGAGTT AAAAATTGCT TTGCCTGAAA TAAGAAGTGC AGAGTTTCTC 205  
 AGAATTCAAA AATGTTCTCA GCTGATTGGA ATTCTACAGT TGAATAATTA AAGAAC 261

## (2) INFORMATION FOR SEQ ID NO:30:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

03702525-033096

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

5 His Lys Lys Pro Asn Gln Pro Ser Arg Pro Ser Asn Thr Ala Ser Lys  
 1 5 10 15  
 Leu Glu Arg Asp Ser Asn Ala Asp Arg Glu Thr Ile Asn Leu Lys Glu  
 20 25 30  
 10 Leu Glu Pro Gln Ile Ala Ser Ala Lys Pro Asn Ala Glu  
 35 40 45

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AAA TGG AAG AAG AAG AAG CGG CCT CGC AAC TCT TAT AAA TGT GGA ACC 48  
 Lys Trp Lys Lys Lys Lys Arg Pro Arg Asn Ser Tyr Lys Cys Gly Thr  
 1 5 10 15  
 AAC ACA ATG GAG AGG GAA GAG AGT GAA CAG ACC AAG AAA AGA GAA AAA 96  
 Asn Thr Met Glu Arg Glu Glu Ser Glu Gln Thr Lys Lys Arg Glu Lys  
 20 25 30  
 40 ATC CAT ATA CCT GAA AGA TCT GAT GAA GCC CAG CGT GTT TTT AAA AGT 144  
 Ile His Ile Pro Glu Arg Ser Asp Glu Ala Gln Arg Val Phe Lys Ser  
 35 40 45  
 45 TCG AAG ACA TCT TCA TGC GAC AAA AGT GAT ACA TGT TTT TAATTAAAGA 193  
 Ser Lys Thr Ser Ser Cys Asp Lys Ser Asp Thr Cys Phe  
 50 55 60  
 GTAAAGCCCA AAAAAAA 210

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

08702525-083095

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

5 Lys Trp Lys Lys Lys Lys Arg Pro Arg Asn Ser Tyr Lys Cys Gly Thr  
 1 5 10 15  
 Asn Thr Met Glu Arg Glu Glu Ser Glu Gln Thr Lys Lys Arg Glu Lys  
 20 25 30  
 10 Ile His Ile Pro Glu Arg Ser Asp Glu Ala Gln Arg Val Phe Lys Ser  
 35 40 45  
 Ser Lys Thr Ser Ser Cys Asp Lys Ser Asp Thr Cys Phe  
 50 55 60

## 15 (2) INFORMATION FOR SEQ ID NO:33:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 359 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 249..359

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GAGTTTTATA CCTCAATAGA CTCTTACTAG TTTCTCTTTT TCAGGTTGTG AAACCTCAACC 60  
 35 TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG 120  
 TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTTGT GAGCCTAGGA 180  
 40 GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTC TCAAAGCAT 240  
 CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC 290  
 Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu  
 1 5 10  
 45 AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT 338  
 Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg  
 15 20 25 30  
 50 CTT TCA CAA GTG TCT TCA GAT 359  
 Leu Ser Gln Val Ser Ser Asp  
 35

## 55 (2) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

03702525-033096

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe  
 1 5 10 15  
 Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg Leu Ser  
 20 25 30  
 Gln Val Ser Ser Asp  
 35

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 318..416

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CCAAAGAAAA AGTGATTTGT CATTGCTTTA TAGACTGTAA GAAGAGAACA TCTCAGAAGT 60  
 GGAGTCTTAC CCTGAAATCA AAGGATTTAA AGAAAAAGTG GAATTTTCT TCAGCAAGCT 120  
 GTGAAACTAA ATCCACAACC TTTGGAGACC CAGGAACACC CTCCAATCTC TGTGTGTTTT 180  
 GTAAACATCA CTGGAGGGTC TTCTACGTGA GCAATTGGAT TGTCATCAGC CCTGCCTGTT 240  
 TTGCACCTGG GAAGTGCCCT GGTCTTACTT GGGTCCAAAT TGTGGCTTT CACTTTTGAC 300  
 CCTAAGCATC TGAAGCC ATG GGC CAC ACA CGG AGG CAG GGA ACA TCA CCA 350  
 Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro  
 1 5 10  
 TCC AAG TGT CCA TAC CTG AAT TTC TTT CAG CTC TTG GTG CTG GCT GGT 398  
 Ser Lys Cys Pro Tyr Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly  
 15 20 25  
 CTT TCT CAC TTC TGT TCA 416  
 Leu Ser His Phe Cys Ser  
 30

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids

960330-52520/30

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr  
1 5 10 15  
Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys  
20 25 30

Ser

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 99..113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGAGCAAGCA GACGCGTAAG AGTGGCTCCT GTAGGCAGCA CGGACTTGAA CAACCAGACT 60  
CCTGTAGACG TGTTCCAGAA CTTACGGAAG CACCCACG ATG GAC CCC AGA TGC 113  
Met Asp Pro Arg Cys  
1 5

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met Asp Pro Arg Cys  
1 5

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 base pairs



- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 107..124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

15 CACAGGGTGA AAGCTTTGCT TCTCTGCTGC TGTAACAGGG ACTAGCACAG ACACACGGAT 60  
GAGTGGGGTTC ATTTCCAGAT ATTAGGTCAC AGCAGAAGCA GCCAAA ATG GAT CCC 115  
Met Asp Pro 1  
20 CAG TGC ACT 124  
Gln Cys Thr 5

25 (2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met Asp Pro Gln Cys Thr  
1 5

40 (2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

50 (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 148..195

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

AGGAGCCTTA GGAGGTACGG GGAGCTCGCA AATACTCCTT TTGGTTTATT CTTACCACCT 60

00702525-003096

TGCTTCTGTG TTCCTTGGGA ATGCTGCTGT GCTTATGCAT CTGGTCTCTT TTTGGAGCTA 120

CAGTGGACAG GCATTTGTGA CAGCACT ATG GGA CTG AGT AAC ATT CTC TTT 171  
Met Gly Leu Ser Asn Ile Leu Phe  
1 5

GTG ATG GCC TTC CTG CTC TCT GGT 195  
Val Met Ala Phe Leu Leu Ser Gly  
10 15

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu Leu Ser Gly  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

CCAACATAAC TGAGTCTGGA AA 22

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

CTGGATTCTG ACTCACCTTC A 21

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs

08702525-083095

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

AGGTTAAGAG TGGTAGAGCC A

21

10

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

AATACCATGT ATCCACATG G

21

25

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

CTGAAGCTAT GGCTTGCAAT T

21

40

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

50

TGGCTTCTCT TTCCTTACCT T

21

(2) INFORMATION FOR SEQ ID NO: 49:

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

GCAAATGGTA GATGAGACTG T

21

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

CAACCGAGAA ATCTACCA GT AA

22

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

GCCGGTAACA AGTCTCTTCA

20

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

AAAAGCTCTA TAGCATTCTG TC

22

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

ACTGACTTGG ACAGTTGTTT A

21

5 (2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

TTTGATGGAC AACTTTACTA

20

20 (2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

CAGCTCACTC AGGCTTATGT

20

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

45 AAACAGCATC TGAGATCAGC A

21

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

CTGAGATCAG CAAGACTGTC

20

960E30-52520/80

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a1

## (2) INFORMATION FOR SEQ ID NO: 58:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: oligonucleotide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

CTGAAGCTAT GGCTTGCAAT T

## (2) INFORMATION FOR SEQ ID NO: 59:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: oligonucleotide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

ACAAGTGTCT TCAGATGTTG AT

## (2) INFORMATION FOR SEQ ID NO: 60:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: oligonucleotide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

CTGGATTCTG ACTCACCTTC A

## (2) INFORMATION FOR SEQ ID NO: 61:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: oligonucleotide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

CCAGGTGAAG TCCTCTGACA

## (2) INFORMATION FOR SEQ ID NO: 62:

08702525-083005  
Sub 351

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1417 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 249..884

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GAGTTTTATA CCTCAATAGA CTCTACTAG TTTCTCTTTT TCAGGTTGTG AAACCTCAACC 60  
 TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG 120  
 TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTGTG GAGCCTAGGA 180  
 GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTT TCCAAAGCAT 240  
 CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC 290  
 Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu  
 1 5 10  
 AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT 338  
 Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg  
 15 20 25 30  
 CTT TCA CAA GTG TCT TCA GAT GTT GAT GAA CAA CTG TCC AAG TCA GTG 386  
 Leu Ser Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val  
 35 35 40 45  
 AAA GAT AAG GTA TTG CTG CCT TGC CGT TAC AAC TCT CCT CAT GAA GAT 434  
 Lys Asp Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp  
 40 50 55 60  
 GAG TCT GAA GAC CGA ATC TAC TGG CAA AAA CAT GAC AAA GTG GTG CTG 482  
 Glu Ser Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu  
 65 70 75  
 TCT GTC ATT GCT GGG AAA CTA AAA GTG TGG CCC GAG TAT AAG AAC CGG 530  
 Ser Val Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg  
 80 85 90  
 ACT TTA TAT GAC AAC ACT ACC TAC TCT CTT ATC ATC CTG GGC CTG GTC 578  
 Thr Leu Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val  
 95 100 105 110  
 CTT TCA GAC CGG GGC ACA TAC AGC TGT GTC GTT CAA AAG AAG GAA AGA 626  
 Leu Ser Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg  
 115 120 125  
 GGA ACG TAT GAA GTT AAA CAC TTG GCT TTA GTA AAG TTG TCC ATC AAA 674  
 Gly Thr Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys  
 130 135 140

0870252430096

5 CCC CCA GAA GAC CCT CCT GAT AGC AAG AAC ACA CTT GTG CTC TTT GGG 722  
Pro Pro Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly  
145 150 155

10 GCA GGA TTC GGC GCA GTA ATA ACA GTC GTC GTC ATC GTT GTC ATC ATC 770  
Ala Gly Phe Gly Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile  
160 165 170

15 AAA TGC TTC TGT AAG CAC AGA AGC TGT TTC AGA AGA AAT GAG GCA AGC 818  
Lys Cys Phe Cys Lys His Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser  
175 180 185 190

20 AGA GAA ACA AAC AAC AGC CTT ACC TTC GGG CCT GAA GAA GCA TTA GCT 866  
Arg Glu Thr Asn Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala  
195 200 205

25 GAA CAG ACC GTC TTC CTT TAGTTCTTCT CTGTCCATGT GGGATACATG GTATTATGTG 924  
Glu Gln Thr Val Phe Leu  
210

30 GCTCATGAGG TACAATCTTT CTTTCAGCAC CGTGCTAGCT GATCTTTCGG ACAACTTGAC 984

35 ACAAGATAGA GTTAACTGGG AAGAGAAAGC CTTGAATGAG GATTTCTTTC CATCAGGAAG 1044

40 CTACGGGCAA GTTTGCTGGG CCTTTGATTG CTTGATGACT GAAGTGGAAA GGCTGAGCCC 1104

45 ACTGTGGGTG GTGCTAGCCC TGGGCAGGGG CAGGTGACCC TGGGTGGTAT AAGAAAAAGA 1164

50 GCTGTCACTA AAAGGAGAGG TGCCTAGTCT TACTGCAACT TGATATGTCA TGTTTGTTG 1224

55 GTGTCTGTGG GAGGCCTGCC CTTTCTGAA GAGAAGTGGT GGCAGAGTGG ATGGGGTGGG 1284

60 GGCAGAGGAA AAGTGGGGGA GAGGCCTGG GAGGAGAGGA GGGAGGGGGA CGGGGTGGGG 1344

65 GTGGGGAAAA CTATGGTTGG GATGTAAAAA CGGATAATAA TATAAATATT AAATAAAAAG 1404

70 AGAGTATTGA GCA 1417

## (2) INFORMATION FOR SEQ ID NO:63:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe  
1 5 10 15

Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg Leu Ser  
20 25 30

Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val Lys Asp  
35 40 45

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Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp Glu Ser  
50 55 60

5 Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu Ser Val  
65 70 75 80

Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg Thr Leu  
85 90 95

10 Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val Leu Ser  
100 105 110

15 Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg Gly Thr  
115 120 125

Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys Pro Pro  
130 135 140

20 Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly  
145 150 155 160

Phe Gly Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys  
165 170 175

25 Phe Cys Lys His Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser Arg Glu  
180 185 190

30 Thr Asn Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln  
195 200 205

Thr Val Phe Leu  
210

35

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1606 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 249..926

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GAGTTTATA CCTCAATAGA CTCTTACTAG TTTCTCTTTT TCAGGTTGTG AAACCTCAACC 60  
55 TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG 120  
TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTGT GAGCCTAGGA 180  
GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTC TCCAAAGCAT 240

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9603303096

	CTGAAGCT	ATG	GCT	TGC	AAT	TGT	CAG	TTG	ATG	CAG	GAT	ACA	CCA	CTC	CTC	290	
	Met	Ala	Cys	Asn	Cys	Gln	Leu	Met	Gln	Asp	Thr	Pro	Leu	Leu			
	1					5					10						
5	AAG	TTT	CCA	TGT	CCA	AGG	CTC	AAT	CTT	CTC	TTT	GTG	CTG	CTG	ATT	CGT	338
	Lys	Phe	Pro	Cys	Pro	Arg	Leu	Asn	Leu	Leu	Phe	Val	Leu	Leu	Ile	Arg	
	15					20					25					30	
10	CTT	TCA	CAA	GTG	TCT	TCA	GAT	GTT	GAT	GAA	CAA	CTG	TCC	AAG	TCA	GTG	386
	Leu	Ser	Gln	Val	Ser	Ser	Asp	Val	Asp	Glu	Gln	Leu	Ser	Lys	Ser	Val	
					35					40					45		
15	AAA	GAT	AAG	GTA	TTG	CTG	CCT	TGC	CGT	TAC	AAC	TCT	CCT	CAT	GAA	GAT	434
	Lys	Asp	Lys	Val	Leu	Leu	Pro	Cys	Arg	Tyr	Asn	Ser	Pro	His	Glu	Asp	
				50					55					60			
20	GAG	TCT	GAA	GAC	CGA	ATC	TAC	TGG	CAA	AAA	CAT	GAC	AAA	GTG	GTG	CTG	482
	Glu	Ser	Glu	Asp	Arg	Ile	Tyr	Trp	Gln	Lys	His	Asp	Lys	Val	Val	Leu	
				65				70					75				
25	TCT	GTC	ATT	GCT	GGG	AAA	CTA	AAA	GTG	TGG	CCC	GAG	TAT	AAG	AAC	CGG	530
	Ser	Val	Ile	Ala	Gly	Lys	Leu	Lys	Val	Trp	Pro	Glu	Tyr	Lys	Asn	Arg	
		80					85					90					
30	ACT	TTA	TAT	GAC	AAC	ACT	ACC	TAC	TCT	CTT	ATC	ATC	CTG	GGC	CTG	GTC	578
	Thr	Leu	Tyr	Asp	Asn	Thr	Thr	Tyr	Ser	Leu	Ile	Ile	Leu	Gly	Leu	Val	
		95				100					105					110	
35	CTT	TCA	GAC	CGG	GGC	ACA	TAC	AGC	TGT	GTC	GTT	CAA	AAG	AAG	GAA	AGA	626
	Leu	Ser	Asp	Arg	Gly	Thr	Tyr	Ser	Cys	Val	Val	Gln	Lys	Lys	Glu	Arg	
					115					120					125		
40	GGA	ACG	TAT	GAA	GTT	AAA	CAC	TTG	GCT	TTA	GTA	AAG	TTG	TCC	ATC	AAA	674
	Gly	Thr	Tyr	Glu	Val	Lys	His	Leu	Ala	Leu	Val	Lys	Leu	Ser	Ile	Lys	
				130					135						140		
45	CCC	CCA	GAA	GAC	CCT	CCT	GAT	AGC	AAG	AAC	ACA	CTT	GTG	CTC	TTT	GGG	722
	Pro	Pro	Glu	Asp	Pro	Pro	Asp	Ser	Lys	Asn	Thr	Leu	Val	Leu	Phe	Gly	
			145					150					155				
50	GCA	GGA	TTC	GGC	GCA	GTA	ATA	ACA	GTC	GTC	GTC	ATC	GTT	GTC	ATC	ATC	770
	Ala	Gly	Phe	Gly	Ala	Val	Ile	Thr	Val	Val	Val	Ile	Val	Val	Ile	Ile	
			160				165					170					
55	AAA	TGC	TTC	TGT	AAG	CAC	GGT	CTC	ATC	TAC	CAT	TTG	CAA	CTG	ACC	TCT	818
	Lys	Cys	Phe	Cys	Lys	His	Gly	Leu	Ile	Tyr	His	Leu	Gln	Leu	Thr	Ser	
						180					185					190	
60	TCT	GCA	AAG	GAC	TTC	AGA	AAC	CTA	GCA	CTA	CCC	TGG	CTC	TGC	AAA	CAC	866
	Ser	Ala	Lys	Asp	Phe	Arg	Asn	Leu	Ala	Leu	Pro	Trp	Leu	Cys	Lys	His	
					195					200					205		
65	GGT	TCT	CTA	GGT	GAA	GCC	TCT	GCA	GTG	ATT	TGC	AGA	AGT	ACT	CAG	ACG	914
	Gly	Ser	Leu	Gly	Glu	Ala	Ser	Ala	Val	Ile	Cys	Arg	Ser	Thr	Gln	Thr	
				210					215						220		

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AAT GAA CCA CAG TAGTTCTGCT GTTCTGAGG ACGTAGTTTA GAGACTGAAT  
 Asn Glu Pro Gln  
 225

966

5 TCTTTGGAAA GGACATAGGG ACAGTTTGCA CATTGCTTG CACATCACAC ACACACACAC 1026  
 ACACACACAC ACACACACAC ACACACACAC ACACACACAC ACACACACAC TCTCTCTCTC 1086  
 10 TCTCTCTCTC GATACCTTAG GATAGGGTTC TACCCTGTTG CTCAGTGACA AAGAATCACT 1146  
 CTGTGGCGGA GGCAGGCTTC AAGCTTGACAG CAATCCTCCT GCACCAGTTT CCTGAGTGCC 1206  
 AGACTTCCAG GTGTAAGCTA TGGCACTTAG CAGAACACTA GCTGAATCAA TGAAGACACT 1266  
 15 GAGGTTCCAA GAGGGAACCT GAATTATGAA GGTGAGTCAG AATCCAGATT TCCTGGCTCT 1326  
 ACCACTCTTA ACCTGTATCT GTTAGACCCC AAGCTCTGAG CTCATAGACA AGCTAATTTA 1386  
 20 AAATGCTTTT TAATAAGCAG AAGGCTCAGT TAGTACGGGG TTCAGGATAC TGCTTACTGG 1446  
 CAATATTTGA CTAGCCTCTA TTTTGTGTTGT TTTTAAAGG CCTACTGACT GTAGTGTAAT 1506  
 TTGTAGGAAA CATGTTGCTA TGTATACCCA TTTGAGGGTA ATAAAAATGT TGGTAATTTT 1566  
 25 CAGCCAGCAC TTTCCAGGTA TTTCCCTTTT TATCCTTCAT 1606

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 226 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

40 Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe  
 1 5 10 15  
 Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg Leu Ser  
 20 25 30  
 45 Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val Lys Asp  
 35 40 45  
 Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp Glu Ser  
 50 55 60  
 Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu Ser Val  
 65 70 75 80  
 55 Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg Thr Leu  
 85 90 95  
 Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val Leu Ser  
 100 105 110

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 960E80-52520/80

- 96 -

Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg Gly Thr  
115 120 125

5 Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys Pro Pro  
130 135 140

Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly  
145 150 155 160

10 Phe Gly Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys  
165 170 175

Phe Cys Lys His Gly Leu Ile Tyr His Leu Gln Leu Thr Ser Ser Ala  
180 185 190

Lys Asp Phe Arg Asn Leu Ala Leu Pro Trp Leu Cys Lys His Gly Ser  
195 200 205

20 Leu Gly Glu Ala Ser Ala Val Ile Cys Arg Ser Thr Gln Thr Asn Glu  
210 215 220

Pro Gln  
225

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